

SEQUENCE LISTING

<110> Turner, C. Alexander Jr.
Mathur, Brian

<120> Novel Human Kinases and Polynucleotides Encoding the Same

<130> LEX-0300-USA

<150> US 60/263,378

<151> 2001-01-23

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2007

<212> DNA

<213> homo sapiens

<400> 1

```
atgacatcga cggggaagga cggcggcgc cagcacgcgc agtatgttgg gccctaccgg 60
ctggagaaga cgtcgggcaa ggggcagaca ggtctggtga agctgggggt tcaactgcgtc 120
acctgccaga aggtggccat caagatcgtc aacctgaga agctcagcga gtcggtgctg 180
atgaaggctg agcgggagat cgcgatcctg aagctcattg agcaccccca cgtccctaaag 240
ctgcacgacg tttatgaaaa caaaaaatat ttgtacctgg tgctagaaca cgtgtcaggt 300
ggtagctctc tgcactacct ggtgaagaag gggaggctga cgctaagga ggctcggaag 360
ttcttcggcg agatcatctc tgcgtcggac ttctgccaca gccactccat atgccacagg 420
gatctgaaac ctgaaaacct cctgctggag gagaagaaca acatccgcgt cgcacacttt 480
ggcatggcgt ccctgcaggt tggcgacagc ctgttgaga ccagctgtgg gtccccccac 540
tacgcctgcc ccgaggtgat ccggggggag aagtatgacg gccggaagcg ggacgtgtgg 600
agctcggcgg tcactcctgt cgccttgctg gtgggggctc tgcccttcga cgtatgacac 660
ttgcgacagc tgcctggaga ggtgaagcgg ggcgtgttcc acatgccgca ctttatcccg 720
ccgactgcc agagtctgct acggggcatg atcagagtg gacggcgacg ccgcctcacg 780
ctagagcaca ttcgaaacaa catatggtat atagggggca agaatagacc gaaccagag 840
cagcccatcc tcgcgaaggt gcagatccgc tcgctgccca gccctggagg catcgacccc 900
gacgtgtctg acagcatgca ctcaactggc tgcctccgag accgcaacaa gctgctgcag 960
gaacctgctg ccgaggagga gaaccaggag aagatgattt acttccctct cctggaccgg 1020
aaagaaaggt acccgagcca ggaggtatga gacctgcccc ccgggaacga gatagacctt 1080
ccccggaagc gtgtggacct cccgatgctg aaccggcacg ccaagcgccg gccagaacgc 1140
aaatccatgg aggtgtctag cgtgacggag ggcggctccc cgggtgcctc gcggcgggcc 1200
attgatagtg ccagcagcgg ccagagggtc cggtccatca cgggtgcctc ctaaggcctt 1260
tccacagacc cactcagcag ccccggggtg accctcacc cctcaccaag gggcagctcc 1320
ctcccccccc ccaaggggac acctgtccac acgccccaa gaggccccgc tggcacgccc 1380
aacccccagc ccccgctcag ccccgagcgt ggagggggtc cctggagggc gcggtctaac 1440
tccatcaaga acagctttct gggctcacc cgtctccacc gccggaaact gcaagttccg 1500
acgcgggagg agatgtccaa cctgacacca gactcgtccc cagagctggc gaagaagctt 1560
tggtttggga acttcacag cctggagaag gaggagcaga tctctgtggt catcaaagac 1620
aaacctctga gctccatcaa ggtgacatc gtgcacgctt tctgtcgat tcccagttct 1680
agccacagcg tcatctccca aacgagcttc cgggcccagt caaagggcca gggggggcca 1740
gcgtgttccc agaagccggt caagtccag gttgatatca cctacacgga ggggtgggag 1800
gcgcagaagg agaaccgcat ctactccgtc acctccacc tgctctcagg cccacgcgtt 1860
cgcttcaaga ggggtgttga gaccatccag gccacgtgct tgagcacaca cgaccgcctt 1920
gcggccacag acctgtcaga caccactaac tgtatggaaa tgatgacggg gcggtttccc 1980
```

aaatgtggaa ttatcccgaa aagttaa

2007

<210> 2

<211> 668

<212> PRT

<213> homo sapiens

<400> 2

```

Met Thr Ser Thr Gly Lys Asp Gly Gly Ala Gln His Ala Gln Tyr Val
 1          5          10          15
Gly Pro Tyr Arg Leu Glu Lys Thr Leu Gly Lys Gly Gln Thr Gly Leu
 20          25          30
Val Lys Leu Gly Val His Cys Val Thr Cys Gln Lys Val Ala Ile Lys
 35          40          45
Ile Val Asn Arg Glu Lys Leu Ser Glu Ser Val Leu Met Lys Val Glu
 50          55          60
Arg Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro His Val Leu Lys
 65          70          75          80
Leu His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr Leu Val Leu Glu
 85          90          95
His Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val Lys Lys Gly Arg
100          105          110
Leu Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln Ile Ile Ser Ala
115          120          125
Leu Asp Phe Cys His Ser His Ser Ile Cys His Arg Asp Leu Lys Pro
130          135          140
Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn Ile Arg Ile Ala Asp Phe
145          150          155          160
Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys
165          170          175
Gly Ser Pro His Tyr Ala Cys Pro Glu Val Ile Arg Gly Glu Lys Tyr
180          185          190
Asp Gly Arg Lys Ala Asp Val Trp Ser Cys Gly Val Ile Leu Phe Ala
195          200          205
Leu Leu Val Gly Ala Leu Pro Phe Asp Asp Asp Asn Leu Arg Gln Leu
210          215          220
Leu Glu Lys Val Lys Arg Gly Val Phe His Met Pro His Phe Ile Pro
225          230          235          240
Pro Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu Val Asp Ala Ala
245          250          255
Arg Arg Leu Thr Leu Glu His Ile Gln Lys His Ile Trp Tyr Ile Gly
260          265          270
Gly Lys Asn Glu Pro Glu Pro Glu Gln Pro Ile Pro Arg Lys Val Gln
275          280          285
Ile Arg Ser Leu Pro Ser Leu Glu Asp Ile Asp Pro Asp Val Leu Asp
290          295          300
Ser Met His Ser Leu Gly Cys Phe Arg Asp Arg Asn Lys Leu Leu Gln
305          310          315          320
Asp Leu Leu Ser Glu Glu Glu Asn Gln Glu Lys Met Ile Tyr Phe Leu
325          330          335
Leu Leu Asp Arg Lys Glu Arg Tyr Pro Ser Gln Glu Asp Glu Asp Leu
340          345          350
Pro Pro Arg Asn Glu Ile Asp Pro Pro Arg Lys Arg Val Asp Ser Pro
355          360          365
Met Leu Asn Arg His Gly Lys Arg Arg Pro Glu Arg Lys Ser Met Glu
370          375          380

```

Val Leu Ser Val Thr Asp Gly Gly Ser Pro Val Pro Ala Arg Arg Ala
 385 390 395 400
 Ile Glu Met Ala Gln His Gly Gln Arg Ser Arg Ser Ile Ser Gly Ala
 405 410 415
 Ser Ser Gly Leu Ser Thr Ser Pro Leu Ser Ser Pro Arg Val Thr Pro
 420 425 430
 His Pro Ser Pro Arg Gly Ser Pro Leu Pro Thr Pro Lys Gly Thr Pro
 435 440 445
 Val His Thr Pro Lys Glu Ser Pro Ala Gly Thr Pro Asn Pro Thr Pro
 450 455 460
 Pro Ser Ser Pro Ser Val Gly Gly Val Pro Trp Arg Ala Arg Leu Asn
 465 470 475 480
 Ser Ile Lys Asn Ser Phe Leu Gly Ser Pro Arg Phe His Arg Arg Lys
 485 490 495
 Leu Gln Val Pro Thr Pro Glu Glu Met Ser Asn Leu Thr Pro Glu Ser
 500 505 510
 Ser Pro Glu Leu Ala Lys Lys Ser Trp Phe Gly Asn Phe Ile Ser Leu
 515 520 525
 Glu Lys Glu Glu Gln Ile Phe Val Val Ile Lys Asp Lys Pro Leu Ser
 530 535 540
 Ser Ile Lys Ala Asp Ile Val His Ala Phe Leu Ser Ile Pro Ser Leu
 545 550 555 560
 Ser His Ser Val Ile Ser Gln Thr Ser Phe Arg Ala Glu Tyr Lys Ala
 565 570 575
 Thr Gly Gly Pro Ala Val Phe Gln Lys Pro Val Lys Phe Gln Val Asp
 580 585 590
 Ile Thr Tyr Thr Glu Gly Gly Glu Ala Gln Lys Glu Asn Gly Ile Tyr
 595 600 605
 Ser Val Thr Phe Thr Leu Leu Ser Gly Pro Ser Arg Arg Phe Lys Arg
 610 615 620
 Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr His Asp Pro Pro
 625 630 635 640
 Ala Ala Gln His Leu Ser Asp Thr Thr Asn Cys Met Glu Met Met Thr
 645 650 655
 Gly Arg Leu Ser Lys Cys Gly Ile Ile Pro Lys Ser
 660 665

<210> 3

<211> 1827

<212> DNA

<213> homo sapiens

<400> 3

atgaaggtg agcggggagat cgcgactcctg aagctcattg agcaccoccca cgtcctaaag 60
 ctgcacgacg tttatgaaaa caaaaaatat ttgtaccttg tgctagaaca cgtgtcagg 120
 ggtgagctct tcgactacct ggtgaagaag gggaggctga cgcctaagga ggctcggaa 180
 ttcttcggcg agatcatctc tgcgctggac ttctgccaca gccactccat atgccacagg 240
 gatctgaacc ctgaaaacct cctgctggac gagaagaaca acatccgcat cgcagacttt 300
 ggcatggcgt ccttgcagggt tggcgacagc ctgttgagaga ccagctgtgg gtccccccac 360
 tacgctgcgc ccgaggtgat ccggggggag aagtatgacg gccggaagcg ggacgtgtgg 420
 agctgcggcg tcactctgtt cgccttctgt gtgggggctc tgcccttcga cgatgacaac 480
 ttgcgacagc tgcgtggagaa ggtgaagcgg ggcgtgttcc acatgcgcga ctttatcccc 540
 ccgactgcc agagtctgct acggggcatg atcgaggtgg acgcgcgacg ccgcctcacg 600
 ctgagacaca ttcaagaaca catatggtat atagggggca agaatagcc cgaaccagag 660
 cagcccatc ctcgcaaggt gcagatccgc tcgctgccca gcctggagga catcgacccc 720

gacgtgctgg acagcatgca ctactctggc tgettcgag accgcaacaa gctgctgcag 780
 gacgtgctgt ccgaggaggga gaaccaggag aagatgattt acttcctcct cctggaccgg 840
 aaagaaaggt accccgagcca ggaggatgag gacctgcccc cccggaacga gatagaccct 900
 ccccggaagc gtgtggactc cccgatgctg aaccggcacg gcaagcggcg gccagaacgc 960
 aaatccatgg aggtgtctcag cgtgacggac ggcggctccc cgggtgctcg gcggcgggcc 1020
 attgagatgg ccagcagcgg ccagaggtct cgggtccatca cgggtgcttc ctacggcctt 1080
 tccaccagcc cactcagcag ccccggggtg acccctcacc cctaccaag gggcagtcct 1140
 ctccccacc ccaaggggac acctgtccac acgccaaagg agagcccgcg tggcagcgcc 1200
 aacccccacg ccccgctccag ccccgcgctg ggagggggtgc cctggagggc gcggctcaac 1260
 tccatcaaga acagctttct gggctcacc cgcttcacc gcgggaaact gcaagttccg 1320
 acgcccggag agatgtccaa cctgacacca gactcgtccc cagagctgct gaaagaagtc 1380
 tgggttggga acttcatcag cctggagaag gaggagcaga tctctgtgt catcaaaagc 1440
 aaacctcga gctccatcaa ggtcgacatc gtgcacgct tctgtctgat tccagtcctc 1500
 agccacagcg tcatctccca aacgagcttc cgggcccagc acaaggccac gggggggcca 1560
 gcgctgttcc agaagccggt caagttccag gttgatata cctacacgga ggggtggggc 1620
 gcgcagaagg gaaacggcat ctactcgcgc acctcacc cgtcttcagg cccagcgct 1680
 cgcttcaaga ggggtgttga gaccatccag gccacgtgc tgagcacaca cgaccgcct 1740
 gcggccagcg acttgtcaga caccactaac tgtatggaaa tgatgacggg gcggctttcc 1800
 aaatgtgtaa ttatcccgaa aagttaa 1827

<210> 4
 <211> 608
 <212> PRT
 <213> homo sapiens

<400> 4
 Met Lys Val Glu Arg Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro
 1 5 10 15
 His Val Leu Lys Leu His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr
 20 25 30
 Leu Val Leu Glu His Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val
 35 40 45
 Lys Lys Gly Arg Leu Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln
 50 55 60
 Ile Ile Ser Ala Leu Asp Phe Cys His Ser His Ser Ile Cys His Arg
 65 70 75 80
 Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn Ile Arg
 85 90 95
 Ile Ala Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu
 100 105 110
 Glu Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu Val Ile Arg
 115 120 125
 Gly Glu Lys Tyr Asp Gly Arg Lys Ala Asp Val Trp Ser Cys Gly Val
 130 135 140
 Ile Leu Phe Ala Leu Leu Val Gly Ala Leu Pro Phe Asp Asp Asp Asn
 145 150 155 160
 Leu Arg Gln Leu Leu Glu Lys Val Lys Arg Gly Val Phe His Met Pro
 165 170 175
 His Phe Ile Pro Pro Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu
 180 185 190
 Val Asp Ala Ala Arg Arg Leu Thr Leu Glu His Ile Gln Lys His Ile
 195 200 205
 Trp Tyr Ile Gly Gly Lys Asn Glu Pro Glu Pro Glu Gln Pro Ile Pro
 210 215 220
 Arg Lys Val Gln Ile Arg Ser Leu Pro Ser Leu Glu Asp Ile Asp Pro
 225 230 235 240

```

Asp Val Leu Asp Ser Met His Ser Leu Gly Cys Phe Arg Asp Arg Asn
      245      250      255
Lys Leu Leu Gln Asp Leu Leu Ser Glu Glu Asn Gln Glu Lys Met
      260      265      270
Ile Tyr Phe Leu Leu Leu Asp Arg Lys Glu Arg Tyr Pro Ser Gln Glu
      275      280      285
Asp Glu Asp Leu Pro Pro Arg Asn Glu Ile Asp Pro Pro Arg Lys Arg
      290      295      300
Val Asp Ser Pro Met Leu Asn Arg His Gly Lys Arg Arg Pro Glu Arg
      305      310      315      320
Lys Ser Met Glu Val Leu Ser Val Thr Asp Gly Gly Ser Pro Val Pro
      325      330      335
Ala Arg Arg Ala Ile Glu Met Ala Gln His Gly Gln Arg Ser Arg Ser
      340      345      350
Ile Ser Gly Ala Ser Ser Gly Leu Ser Thr Ser Pro Leu Ser Ser Pro
      355      360      365
Arg Val Thr Pro His Pro Ser Pro Arg Gly Ser Pro Leu Pro Thr Pro
      370      375      380
Lys Gly Thr Pro Val His Thr Pro Lys Glu Ser Pro Ala Gly Thr Pro
      385      390      395      400
Asn Pro Thr Pro Pro Ser Ser Pro Ser Val Gly Gly Val Pro Trp Arg
      405      410      415
Ala Arg Leu Asn Ser Ile Lys Asn Ser Phe Leu Gly Ser Pro Arg Phe
      420      425      430
His Arg Arg Lys Leu Gln Val Pro Thr Pro Glu Glu Met Ser Asn Leu
      435      440      445
Thr Pro Glu Ser Ser Pro Glu Leu Ala Lys Lys Ser Trp Phe Gly Asn
      450      455      460
Phe Ile Ser Leu Glu Lys Glu Glu Gln Ile Phe Val Val Ile Lys Asp
      465      470      475      480
Lys Pro Leu Ser Ser Ile Lys Ala Asp Ile Val His Ala Phe Leu Ser
      485      490      495
Ile Pro Ser Leu Ser His Ser Val Ile Ser Gln Thr Ser Phe Arg Ala
      500      505      510
Glu Tyr Lys Ala Thr Gly Gly Pro Ala Val Phe Gln Lys Pro Val Lys
      515      520      525
Phe Gln Val Asp Ile Thr Tyr Thr Glu Gly Gly Glu Ala Gln Lys Glu
      530      535      540
Asn Gly Ile Tyr Ser Val Thr Phe Thr Leu Leu Ser Gly Pro Ser Arg
      545      550      555      560
Arg Phe Lys Arg Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr
      565      570      575
His Asp Pro Pro Ala Ala Gln His Leu Ser Asp Thr Thr Asn Cys Met
      580      585      590
Glu Met Met Thr Gly Arg Leu Ser Lys Cys Gly Ile Ile Pro Lys Ser
      595      600      605

```